

REMARKS

Claims 1-3, 11, and 13-25 are pending in the present application. It appears that the Examiner has examined claims 1-3, 11, 13, 16-20 and 23-24. Claims 14-15, 21-22 and 25 appear to be withdrawn from consideration as being drawn to a non-elected invention. Claims 1 and 17 are independent claims.

Applicants have amended the specification to recite divisional status of this application. Applicants have not raised any issue of new matter.

Foreign Priority

The Examiner reports that foreign priority documents have not been received; however, this application is a Division of U.S. Application 08/676,882, July 3, 1996, now U.S. Patent 6,100,241. The priority documents are in the parent application, but we can easily file a copy of EP 95 201 801.8, filed July 3, 1995.

More importantly, this application should have at least a priority date of the parent application 08/676,882, filed July 3, 1996, because this application is a division of 08/676,882.

Drawings

Applicants will address the issues asserted on form PTO form 948 when the application has been indicated as being allowable.

Issue Under 35 U.S.C. §112

Claims 1-3, 11, 16-20, 23 and 24 stand rejected under 35 U.S.C. §112, first paragraph as allegedly having a specification that enables an isolated 37 kD protein from *Eimeria acervulina* with amino acid sequence set forth in SEQ ID NO: 2 and a vaccine comprising the 37 kD protein, but failing to provide an enabling disclosure for any fragment of the isolated protein.

Applicants traverse this rejection. First of all, Applicants have not claimed "any fragment of the isolated protein." Applicants have clearly claimed: An isolated protein comprising one or more immunoreactive and/or antigenic determinants of *Eimeria* lactate dehydrogenase (LDH), wherein said isolated protein is found intracellularly in *Eimeria*. Only those fragment that are immunoreactive and/or antigenic determinants of *Eimeria* LDH are within the scope of the present invention.

The important terms to a skilled artisan relating to the protein parts that define the present invention are: "immunoreactive and/or antigenic determinants"; "a biologically active variant", and "an immunologically active part"

Immunoreactive and/or antigenic determinants of *Eimeria* lactate dehydrogenase are disclosed on page 6, lines 12 through 15. Detailed definitions are presented on page 8, line 27 through page 9, line 2 of the description. Routine techniques

for determining which fragments are immunogenic determinants are disclosed on page 9, lines 3 through 27. Both PEPSCAN and computer analyses allow the routine prediction of antigenic determinants. An illustration of the effectiveness of using these methods was published by H. Margalit et al. (1987, J. of Immunol., vol. 138, p. 2213-2229) who describe success rates of 75% in the prediction of epitopes using such methods.

Biologically functional equivalents or variants are described on page 7, lines 12 through 16 of the description. Commonly observed protein modifications are disclosed on page 7, lines 4 - 11. The equivalents and variants are defined on page 7, lines 17 through 25. As is specifically stated, such equivalent or variant proteins may be derived by insertions or deletion, but: ". . . retain one or more immunogenic determinants of the Eimeria antigens . . .".

A description of biological functional equivalents, for instance proteins carrying conserved amino acid mutations arising through evolutionary variations between Eimeria strains, is presented on page 7, line 26 through page 8, line 20. As is stated in lines 16-20 on page 8: "Such amino acid substitutions of the exemplary embodiments of this invention are within the scope of the invention as long as the resulting proteins **retain their immunoreactivity**" (emphasis added).

Methods to obtain such fragments are disclosed on page 8 line 27 through page 9, line 2.

An immunologically active part of the protein in SEQ ID NO: 2 can be determined and obtained in ways similar to the immunoreactive and/or antigenic determinants, see above.

Finally, Applicants submit that methods for establishing LDH activity of parts of the Eimeria protein of the invention have been well known in the art for many years. Detection of LDH enzyme activity is a standard technique in clinical chemistry labs in all major hospitals, for instance as a marker for myocardial or other diseases (reviewed by: P. Wolf, 1989, Clin. Lab. Med., vol. 9, p. 655-665).

Interestingly, measurement of LDH activity has also been described as a test for determining Plasmodium parasitemia (M. Makler and D. Hinrichs, 1993, Am. J. Trop. Med. Hyg., vol. 48, p. 205-210). *Abstracts are enclosed.*

"The test of enablement is whether one reasonably skilled in the art could make or use the invention from the disclosures in the patent coupled with information known in the art without undue experimentation." In re Buchner, 929 F.2d 660, 661, 18 U.S.P.Q.2d 1331, 1332 (Fed. Cir. 1991). Also, the MPEP §2164.01 states that "[a] patent need not teach, and preferably omits, what is well known in the art." The determination of immunogenic and/or antigenic fragments of a protein is well known in the art and a skilled artisan would not suffer an undue burden of experimentation in obtaining the claimed scope of the present invention.

Issue Under 35 U.S.C. §102(e)

Claims 1-3, 11, 16-20 and 23-24 stand rejected under 35 U.S.C. §102(e) as being anticipated by Kok '241 (USP 6,100,241). Applicants traverse this rejection.

This rejection is completely improper. Kok '241 is the parent of this application, as Applicants noted in the Response of March 22, 2002 and now stated on the first line and of the first page of the present specification. Therefore, Kok '241 cannot be used as prior art against this application.

Applicants respectfully request withdrawal of the 35 U.S.C. §102 rejection.

Issue Under 35 U.S.C. §102(e)

Claims 1-3, 11, 16-20 and 23-24 stand rejected under 35 U.S.C. §102(e) as being anticipated by Binger '015 (USP 5,661,015). The Examiner asserts that Binger '015 discloses each element of the present invention. Applicants assert that patentable distinction exists between the cited prior art and the present invention.

Distinction Between the Present Invention and Binger '015

Binger '015 discloses DNA sequences coding for Eimeria surface antigens, recombinant vectors containing such DNA sequences, transformed microorganisms containing such vectors, and method for producing the antigens using the transformed microorganisms.

Applicants direct the Examiner to Applicants' response of March 22, 2002 for a discussion on why the 37 kD protein disclosed in Binger '015 is on the surface. Applicants will not repeat this argument here, but still assert the Examiner is erroneous in her assessment of Binger '015.

The Examiner asserts an unjust conclusion: based on the molecular weight and the presence in Eimeria, the Examiner extrapolates the Binger '015 protein to having the same function as the protein of the invention, by stating (on page 7, line 7 of the office action):". . . they appear to possess the same or similar functional characteristics, i.e. LDH activity . . .". This assertion is baseless. More importantly, Applicants can demonstrate that it is untrue. Apart from having an amino acid sequence completely unrelated to the one of the invention, the Binger '015 protein is not an LDH.

For support, Applicants present the following facts. First, Binger '015 fails to disclose the terms Lactate or dehydrogenase anywhere within the patent disclosure. Secondly, Binger '015 fails to disclose a possible function for the protein, let alone

an activity as an enzyme.

Applicants can demonstrate that the Binger '015 protein is not an LDH, by computer analyses that can easily be performed using the program "BlastP" from the NCBI Internet website (URL: <http://www.ncbi.nlm.nih.gov/Blast>), by applying the function for a conserved domain search. For instance, Applicants have performed the following analyses:

An alignment of the protein from seq. id. no. 2 of the present invention with all entries of the complete NCBI protein database shows significant (*) matches to lactate and malate dehydrogenase enzymes, while such an alignment done with the Binger '015 protein (fig. 32) only results in a few non-significant (*) hits to unrelated proteins.

A computer analysis was performed with the protein from Binger '015 and with the protein of the present invention, for amino acid stretches that represent the characteristic conserved domains shared by all (lactate) dehydrogenase enzymes. Such conserved domains are not present in the Binger '015 protein, while very prominent in the protein of the invention (see enclosures Ap 3, and 10).

(*) significance of an alignment-result from the Blast

programs is represented as "E value"; the smaller this is, the less probability exists that the match found occurred by chance. Rule of thumb: significance starts below 0.1, and becomes stronger the smaller the E value gets, ultimately it can be zero for a full and specific match. Compare for instance the high significance of the matches of the seq. id. 2 protein of the invention: $E = 10^{-117}$ through 10^{-39} , to the non-significant (thus accidental) matches found for the Binger protein: $E = 0.3$ through 8.9.

Enclosed are printouts of the results of such analyses:

Enclosure- page(s):	Content:
Ap 1 - 7	Results from analyses with Binger protein
1 - 2	BlastP analysis order form
3	Results from conserved domain search
4 - 7	Results from protein database alignment
Ap 8 - 14	Results from analyses with seq. id. 2 protein
8 - 9	BlastP analysis order form
10	Results from conserved domain search
11 - 12	Description of conserved domains detected
13 - 14	Results from protein database alignment
(partial)	

"A claim is anticipated only if each and every element as set forth in the claim is found, either expressly or inherently described, in a single prior art reference." Verdegaal Bros. v. Union Oil Co. of California, 814 F.2d 628, 631, 2 U.S.P.Q.2d 1051, 1053 (Fed. Cir. 1987). Binger '015 fails to disclose each and every element as set forth in the instant claims. With the

overwhelming evidence that the Binger '015 protein fails to fall within the scope of the present invention, Applicants respectfully request withdrawal of the 35 U.S.C. §102(e) rejection.

Conclusion

All the stated grounds of the rejections have been properly traversed, accommodated or rendered moot. Applicants respectfully submit that the present application is in condition for allowance.

Attached hereto is a marked-up version to show changes to the application by this amendment.

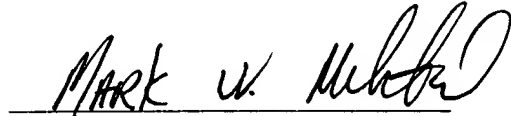
If the Examiner believes for any reason that personal communication will expedite prosecution of this application, the Examiner is invited to telephone the undersigned at (302) 934-4395, in Millsboro, Delaware.

If necessary, the Commissioner is hereby authorized in this, concurrent, and further replies, to charge payment or credit any overpayment to Deposit Account No. 02-2334 for any additional

Attorney Docket NO. I/95150-US/D1

fees required under 37 C.F.R. \$1.16 or under 37 C.F.R. \$1.17;
particularly extension of time fees.

Respectfully submitted,



Mark W. Milstead
Patent Counsel
Registration No. 45,825

Attorney Docket NO. I/95150-US/D1

Intervet Inc.
Patent Department
405 State Street
P.O. Box 318
Millsboro, DE 19966
Tel: (302) 933-4034
Fax: (302) 933-4013

MWM

Enclosure: Version with Markings to Show Changes Made

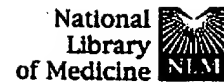
- Abstracts of Wolf and Makler references.
- Alignment result and sequence files of AAW33626 (Binger protein) and seq. id. no. 2.
- Pages Ap 1 - 14, BlastP and Conserved domain search results of both seq. id. 2 and the Binger protein, see description above.

Version with Markings to Show Changes Made

In the Specification:

The following paragraph has been added before the paragraph beginning on page 1 line 1.

--This application is a division of U.S. Application No. 08/676,882, filed July 3, 1996, now U.S. Patent No. 6,100,241.--



PubMed Nucleotide Protein Genome Structure PopSet Taxonomy OMIM

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Abstract



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1: Am J Trop Med Hyg 1993 Feb;48(2):205-10

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Measurement of the lactate dehydrogenase activity of *Plasmodium falciparum* as an assessment of parasitemia.

Makler MT, Hinrichs DJ.

Clinical Pathology and Research Service, Veterans Administration Medical Center, Portland, Oregon.

This report describes an enzyme assay for the detection of *Plasmodium falciparum*. The assay is based on the observation that the lactate dehydrogenase (LDH) enzyme of *P. falciparum* has the ability to rapidly use 3-acetyl pyridine NAD (APAD) as a coenzyme in the reaction leading to the formation of pyruvate from lactate. Human red blood cell LDH carries out this reaction at a very slow rate in the presence of APAD. We measured the development of APADH and found that the formation of the product could establish the basis of an assay that detected the presence of *P. falciparum* from in vitro cultures at parasitemia levels of 0.02%. We also had occasion to use this assay with clinical samples. We found a correlation between levels of parasitemia and the activity of parasite LDH. Parasite LDH (pLDH) activity could be measured in blood hemolysates and in plasma and serum from patients with malaria. We used the serum assay for pLDH and followed the level of pLDH in a patient with cerebral malaria prior to antimalarial treatment and during the recovery period. From these initial studies, it is evident that the measurement of pLDH has correlation with parasitemia and may offer a method that can be developed into a simple test for the detection of *Plasmodium* parasitemia.

PMID: 8447524 [PubMed - indexed for MEDLINE]



Abstract



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Text



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Reference molecule: AAW33626 1 - 178 (178 aa) Homology

Sequence 2: SEQ_ID_2.TXT 1 - 330 (330 aa) 25%

Alignment type: Global Protein

Parameters: Mismatch 2; Open Gap 4; Extend Gap 1; Conserv N

```

AAW33626      (    1) tsreapgaspp-akrrrtslgapaagegpllrweqpaa-----gtaaa-----
SEQ_ID_2.TXT (    1) mavfekntrpkiamvgsgmiggtmaflcsrlrelgdvvlfdvvpnmpmgkamdslnssvv

AAW33626      (   44) -----rqqlleereqqqrqreqqlqhvr
SEQ_ID_2.TXT (   61) dtgitvygsnsyeclkgadvviitagitkipgksdkewsrmddlpvnikimrevgaaiks

AAW33626      (   65) stpgraaavqarlñawvaeognklpese-----nrrmleqymnl----
SEQ_ID_2.TXT (  121) ycp--nairvinitnpldvmvaalqessglphhricgmagmldssnrrmiadklevsprd

AAW33626      (  104) -----ekvkkklrkkldesaearakyiegefkknpchw
SEQ_ID_2.TXT (  179) vqgmvigvhgdhmvplsryatvngiplsefvkkqwikqeevddivqggtkvaggeivrllg

AAW33626      (  136) plkaenpllpfaqreadeayrrf-----grgapsag
SEQ_ID_2.TXT (  239) qgsäyyapgasaiqma-esylkdrkrvmvcscylqggygvqnhylgvpcviggrgvekii

AAW33626      (  167) plrekmlqarr-----k
SEQ_ID_2.TXT (  298) el-eltagerqelqgsidevkemqkaiaaldask

```

AAGENESEQ:AAW33626

ID AAW33626 standard; Protein; 178 AA.

XX

AC AAW33626;

XX

DT 21-MAY-1998 (first entry)

XX

DE Eimeria tenella sporozoite, schizont, merozoite antigen.

XX

KW Coccidiosis; vaccine; poultry; protozoan; parasite; antigen;

KW sporozoite; schizont; merozoite.

XX

OS Eimeria tenella.

XX

FH Key Location/Qualifiers

FT Misc-difference 64

FT /note= "encoded by CAG"

FT Misc-difference 65

FT /note= "encoded by CGC"

XX

PN US5661015-A.

XX

PD 26-AUG-1997.

XX

PF 03-JUN-1988; 88US-0202721.

XX

PR 20-DEC-1991; 91US-0812349.

PR 03-JUN-1988; 88US-0202721.

XX

PA (HOFF) HOFFMANN LA ROCHE INC.

XX

PI Altenburger W, Binger M, Chizzonite RA, Kramer RA;

PI Lomedico PT, McAndrew SJ;

XX

DR WPI; 1997-434379/40.

DR N-PSDB; AAT93598.

XX

PT New DNA from Eimeria tenella and related immunogenic polypeptides -

PT useful in vaccines to protect poultry against coccidiosis

XX

PS Example 6.5; Fig 32; 72pp; English.

XX

CC This 28 kDa protein is recognised by monoclonal antibody 8A2
CC (ATCC HB 9710). This antibody also specifically reacts with an
CC *Eimeria tenella* 37 kDa surface antigen that is present in the
CC sporozoite, schizont and merozoite developmental stages. The
CC amino acid sequence was deduced from a cDNA clone (see AAT93598)
CC obtained from a cDNA library by immunological screening with
CC monoclonal antibodies raised against *Eimeria* antigens. The
CC invention provides DNA sequences (see AAT93593-98) coding for *Eimeria*
CC surface antigens (see AAW31582-84 and AAW33621-26), recombinant vectors
CC containing such DNA sequences, transformed microorganisms
CC containing such vectors, and methods for producing the antigens
CC using the transformed microorganisms. Methods are also provided
CC for protecting poultry against coccidiosis using the *Eimeria*
CC surface antigens. The surface antigens are administered either as
CC purified proteins or in the form of DNA encoding the proteins in a
CC viral vector such as a vaccinia virus. The vaccines may produce
CC antibodies that are cross-reactive with other *Eimeria* species.

XX

SQ Sequence 178 AA;

SQ 27 A; 26 R; 5 N; 2 D; 0 B; 0 C; 13 Q; 21 E; 0 Z; 12 G; 2 H;

SQ 2 I; 15 L; 13 K; 3 M; 3 F; 14 P; 6 S; 4 T; 3 W; 3 Y; 4 V;

SQ 0 Others;

tsreapgasp pakrrrtslg apaagegplr rweqpaagta aairqcleer eqqrqreqql
qhvrstpgra aavqarinaw vaegnklpes errrmleqy mnlekvvklr kkideeae
akyliegefkk nphwgplkae nplpfaqr adeayrrfgr gapsagplre kmlqarrk

//

95150BWP.SEQ1
SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Akzo Nobel N.V.
- (B) STREET: Velperweg 76
- (C) CITY: Arnhem
- (E) COUNTRY: The Netherlands
- (F) POSTAL CODE (ZIP): 6824 BM
- (G) TELEPHONE: 04120-66204
- (H) TELEFAX: 04120-50592
- (I) TELEX: 37503 akpha nl

(ii) TITLE OF INVENTION: T cell stimulatory protein of Eimeria

(iii) NUMBER OF SEQUENCES: 2

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1679 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Eimeria acervulina
- (D) DEVELOPMENTAL STAGE: Schizont

(vii) IMMEDIATE SOURCE:

- (B) CLONE: EASC2_1

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 280..1269
- (D) OTHER INFORMATION: /function= "Eimeria lactate dehydrogenase"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: /label= pBluescriptII

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1624..1679
- (D) OTHER INFORMATION: /label= pBluescriptII

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 45..54
- (D) OTHER INFORMATION: /label= EcoRI-linker

95150BWP.SEQ1

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION:1621..1630
 (D) OTHER INFORMATION:/label= EcoRI-linker

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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TTTTTTTCT ACACATTAAT ATTCTTCGTT TACGTTTATT TTGCTACAAA TAAACCCCTT      120
AAACTCTCTA TTTCCTCATA TTCTACCGCT TCATCGGTGG GTGTGTAAGA CGTACGTACG      180
TACAGCTGGG GCTGGCTTAC TGCGCACCGC TTATTTATTA CTTAATTCAT ACACATTTTA      240
TATCTTTCTT CTTCCTTTT CTGCTCTTT CTTGTGAAA ATG GCG GTC TTC GAG      294
                               Met Ala Val Phe Glu
                               1           5

AAG AAT ACA CGC CCC AAG ATT GCT ATG GTG GGC TCC GGT ATG ATT GGA      342
Lys Asn Thr Arg Pro Lys Ile Ala Met Val Gly Ser Gly Met Ile Gly
                               10           15           20

GGC ACC ATG GCT TTC CTG TGC AGC TTG AGG GAA CTC GGA GAT GTT GTC      390
Gly Thr Met Ala Phe Leu Cys Ser Leu Arg Glu Leu Gly Asp Val Val
                               25           30           35

CTC TTC GAC GTT GTA CCG AAC ATG CCG ATG GGG AAG GCG ATG GAT ATA      438
Leu Phe Asp Val Val Pro Asn Met Pro Met Gly Lys Ala Met Asp Ile
                               40           45           50

TCG CAC AAT TCG TCG GTG GTT GAC ACG GGT ATA ACA GTA TAC GGC TCA      486
Ser His Asn Ser Ser Val Val Asp Thr Gly Ile Thr Val Tyr Gly Ser
                               55           60           65

AAT TCA TAC GAG TGC TTG AAG GGT GCG GAC GTA GTA ATA ATA ACA GCA      534
Asn Ser Tyr Glu Cys Leu Lys Gly Ala Asp Val Val Ile Ile Thr Ala
                               70           75           80           85

GGG ATA ACA AAG ATA CCC GGA AAG AGC GAT AAA GAA TGG TCT AGA ATG      582
Gly Ile Thr Lys Ile Pro Gly Lys Ser Asp Lys Glu Trp Ser Arg Met
                               90           95           100

GAT CTA TTA CCT GTG AAT ATA AAG ATA ATG AGG GAG GTC GGT GCA GCA      630
Asp Leu Leu Pro Val Asn Ile Lys Ile Met Arg Glu Val Gly Ala Ala
                               105          110          115

ATT AAA TCT TAC TGT CCT AAT GCA TTT GTT ATT AAT ATA ACA AAT CCT      678
Ile Lys Ser Tyr Cys Pro Asn Ala Phe Val Ile Asn Ile Thr Asn Pro
                               120          125          130

TTA GAT GTG ATG GTA GCT GCT CTT CAA GAG TCA TCA GGA CTA CCT CAT      726
Leu Asp Val Met Val Ala Ala Leu Gln Glu Ser Ser Gly Leu Pro His
                               135          140          145

CAT AGA ATC TGC GGT ATG GCT GGG ATG CTT GAT AGC TCT CGT TTT AGA      774
His Arg Ile Cys Gly Met Ala Gly Met Leu Asp Ser Ser Arg Phe Arg
                               150          155          160          165

CGT ATG ATA GCT GAT AAA TTA GAA GTC TCT CCT AGA GAT GTA CAG GGG      822
Arg Met Ile Ala Asp Lys Leu Glu Val Ser Pro Arg Asp Val Gln Gly
                               170          175          180

ATG GTC ATA GGT GTA CAC GGC GAT CAT ATG GTG CCC CTA AGT AGA TAT      870
Met Val Ile Gly Val His Gly Asp His Met Val Pro Leu Ser Arg Tyr
                               185          190          195

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95150BWP.SEQ1

GCA ACA GTT AAC GGC ATC CCG CTT TCT GAG TTT GTT AAG AAG GGC TGG	918
Ala Thr Val Asn Gly Ile Pro Leu Ser Glu Phe Val Lys Lys Gly Trp	
200 205 210	
ATC AAG CAA GAA GAA GTA GAT GAT ATC GTT CAG AAG ACC AAG GTC GCT	966
Ile Lys Gln Glu Glu Val Asp Asp Ile Val Gln Lys Thr Lys Val Ala	
215 220 225	
GGA GGA GAG ATC GTA CGC CTA TTA GGA CAA GGC TCT GCT TAC TAT GCT	1014
Gly Gly Glu Ile Val Arg Leu Leu Gly Gln Gly Ser Ala Tyr Tyr Ala	
230 235 240 245	
CCA GGG GCT TCA GCT ATT CAG ATG GCT GAG AGC TAT CTA AAG GAT AGA	1062
Pro Gly Ala Ser Ile Glu Met Ala Glu Ser Tyr Leu Lys Asp Arg	
250 255 260	
AAG AGA GTG ATG GTT TGC TCT TGC TAC TTG CAA GGA CAA TAT GGT GTA	1110
Lys Arg Val Met Val Cys Ser Cys Tyr Leu Gln Gly Gln Tyr Gly Val	
265 270 275	
CAG AAT CAC TAC TTA GGA GTA CCT TGT GTT ATC GGT GGG AGA GGT GTT	1158
Gln Asn His Tyr Leu Gly Val Pro Cys Val Ile Gly Gly Arg Gly Val	
280 285 290	
GAG AAG ATT ATT GAG TTA GAA TTG ACC GCA CAA GAA AGA CAG GAG CTT	1206
Glu Lys Ile Ile Glu Leu Glu Leu Thr Ala Gln Glu Arg Gln Glu Leu	
295 300 305	
CAG GGA TCT ATC GAT GAG GTT AAG GAG ATG CAG AAG GCT ATT GCT GCT	1254
Gln Gly Ser Ile Asp Glu Val Lys Glu Met Gln Lys Ala Ile Ala Ala	
310 315 320 325	
CTT GAT GCA TCC AAG TAAGCAGCAG CAAAATCGCA GAAGTTGCAG CGCTAGAACA	1309
Leu Asp Ala Ser Lys	
330	
ACCAGCAGCA GCAGCAGCAG CAGCCTATAG TTCTTGCTGC TGCTGTTCTT ACTACAGCTG	1369
CGGCTTTCTT CCTCGTGTTA TTATCATGAT AGTAAGCTGC TGTACCAGCA GCAGCAGCAG	1429
CAGCAGATTT TGCTTGACCC GCCGTTTGTT TTGCGTACAC CGGCAGAAAT ATTGACTTGC	1489
AGTTAGGAGA AAGAAAGAAA ACAAACACGA TCCCATCGAT CCAAATAAAC CCCACACTGT	1549
CGATCCCATC GATCCACGCA ACTCCACGGG GCTCTTAACT GTTAAACCTA TTATTCTTAT	1609
CATTACTGTC TCCCGAATTC GATATCAAGC TTATCGATAC CGTCGACCTC GAGGGGGGGC	1669
CCGGTACCCA	1679

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Ala	Val	Phe	Glu	Lys	Asn	Thr	Arg	Pro	Lys	Ile	Ala	Met	Val	Gly
1				5					10					15	
Ser	Gly	Met	Ile	Gly	Gly	Thr	Met	Ala	Phe	Leu	Cys	Ser	Leu	Arg	Glu
		20						25					30		
Leu	Gly	Asp	Val	Val	Leu	Phe	Asp	Val	Val	Pro	Asn	Met	Pro	Met	Gly

951508WP.SEQ1

35 40 45
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 50 55 60
 Thr Val Tyr Gly Ser Asn Ser Tyr Glu Cys Leu Lys Gly Ala Asp Val
 65 70 75 80
 Val Ile Ile Thr Ala Gly Ile Thr Lys Ile Pro Gly Lys Ser Asp Lys
 85 90 95
 Glu Trp Ser Arg Met Asp Leu Leu Pro Val Asn Ile Lys Ile Met Arg
 100 105 110
 Glu Val Gly Ala Ala Ile Lys Ser Tyr Cys Pro Asn Ala Phe Val Ile
 115 120 125
 Asn Ile Thr Asn Pro Leu Asp Val Met Val Ala Ala Leu Gln Glu Ser
 130 135 140
 Ser Gly Leu Pro His His Arg Ile Cys Gly Met Ala Gly Met Leu Asp
 145 150 155 160
 Ser Ser Arg Phe Arg Arg Met Ile Ala Asp Lys Leu Glu Val Ser Pro
 165 170 175
 Arg Asp Val Gln Gly Met Val Ile Gly Val His Gly Asp His Met Val
 180 185 190
 Pro Leu Ser Arg Tyr Ala Thr Val Asn Gly Ile Pro Leu Ser Glu Phe
 195 200 205
 Val Lys Lys Gly Trp Ile Lys Gln Glu Glu Val Asp Asp Ile Val Gln
 210 215 220
 Lys Thr Lys Val Ala Gly Gly Glu Ile Val Arg Leu Leu Gly Gln Gly
 225 230 235 240
 Ser Ala Tyr Tyr Ala Pro Gly Ala Ser Ala Ile Gln Met Ala Glu Ser
 245 250 255
 Tyr Leu Lys Asp Arg Lys Arg Val Met Val Cys Ser Cys Tyr Leu Gln
 260 265 270
 Gly Gln Tyr Gly Val Gln Asn His Tyr Leu Gly Val Pro Cys Val Ile
 275 280 285
 Gly Gly Arg Gly Val Glu Lys Ile Ile Glu Leu Glu Leu Thr Ala Gln
 290 295 300
 Glu Arg Gln Glu Leu Gln Gly Ser Ile Asp Glu Val Lys Glu Met Gln
 305 310 315 320
 Lys Ala Ile Ala Ala Leu Asp Ala Ser Lys
 325 330



Nucleotide

Protein

protein-protein

Translations

BLASTRetrieve results for an
RID[Search](#)

tsreapgasppakrrrtslgapaagegplrrweqpaagtaaaairqqleereqqrreq
ql
qhvrrstpgraaavqarlrawaegnklpeserrrrmleqymnlekvkklrkkldeae
ar
akyiegefkknpwhgplkaenpllpfaqreadeayrrfgrgapsagplrekmlqarrk

Set subsequence From: To: Choose database Do CD-Search ☒Now: **BLAST!** or **Reset query** **Reset all****Options** for advanced blastingLimit by [entrez query](#) or select from: [Composition-based statistics](#) ☒Choose filter ☒ Low complexity ☐ Mask for lookup table only ☐ Mask lower caseExpect Word Size Matrix Gap Costs [PSSM](#)[Other advanced](#) [PHI pattern](#)

Ap 2.

FormatShow ☒ Graphical Overview ☒ Linkout ☒ NCBI-gi Alignment ☒ in HTML ☒ formatNumber of: Descriptions ☒ Alignments ☒Alignment view ☒Format for PSI-
BLAST ☐ with inclusion threshold: Limit results by or select from: ☒Expect value
range: Layout: ☒ Formatting options on page with results: ☒Autoformat ☒**BLAST!** or **Reset all**Get the URL with preset values ? **Get URL**



Nucleotide

Protein

formatting **BLAST**

Translations

Retrieve results for an
RID

Your request has been successfully submitted and put into the Blast Queue.

Query = (178 letters)

No putative conserved domains have been detected

The request ID is 1031904890-06049-27032

Format! or **Reset all**

The results are estimated to be ready in 9 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show ☒ Graphical Overview ☒ Linkout ☒ NCBI-gi Alignment ☒ in format

Number of: Descriptions Alignments

Alignment view

Format for PSI-BLAST ☐ with inclusion threshold:

Limit results by or select from:

Expect value range:



results of BLAST

BLASTP 2.2.4 [Aug-26-2002]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1031904190-027664-9746

Query=

(178 letters)

Database: All non-redundant GenBank CDS

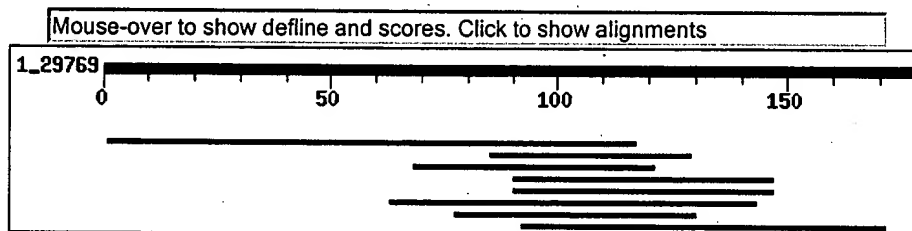
translations+PDB+SwissProt+PIR+PRF

1,044,513 sequences; 330,426,180 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 8 Blast Hits on the Query Sequence



Sequences producing significant alignments:

	Score	E	
	(bits)	Value	
gi 3309614 gb AAC26124.1 (AF073462) serine rich protein [E...	<u>35</u>	0.30	
gi 17508897 ref NP_492564.1 (NM_060163) T05F1.11.p [Caenor...	<u>35</u>	0.30	L
gi 19115578 ref NP_594666.1 (NC_003424) putative DNA repai...	<u>34</u>	0.61	
gi 20349350 ref XP_112453.1 (XM_112453) similar to hypothe...	<u>32</u>	2.9	L
gi 20888303 ref XP_146514.1 (XM_146514) similar to hypothe...	<u>32</u>	2.9	L
gi 20837540 ref XP_130281.1 (XM_130281) similar to oxyster...	<u>31</u>	5.3	L
gi 12025422 gb AAG45917.1 AF309776.1 (AF309776) guanylyl cy...	<u>31</u>	7.8	
gi 6739527 gb AAF27289.1 AF140613.1 (AF140613) N-hydroxylat...	<u>30</u>	8.9	

Alignments

[Get selected sequences](#) [Select all](#) [Deselect all](#)

┌>gi|3309614|gb|AAC26124.1| (AF073462) serine rich protein [Eimeria acervulina]
Length = 271

Score = 35.4 bits (80), Expect = 0.30

Identities = 39/128 (30%), Positives = 57/128 (44%), Gaps = 11/128 (8%)

Query: 2 SREAPGASPPAKRRRTS-----LGAPAAGEGPLRRWEQ----PAAGTAAAIXXXXXX 50
S PG S ++R S A +G P RR + P +G A
Sbjct: 131 SSPQPGPSAGTRKRPPSDAAARYLAAAEGSGGSPKRRRVETRGMPPSGLVKARSQDAEDR 190

Query: 51 XXXXXXXXXXXXHVRSTPGRAAAVQARLNAWVAEGNKLPESERRRRMLEQYMNLEKVKKLR 110
+V TPG+A V+ L + V EGNK E +RR ML++YM+ +V++ R
Sbjct: 191 DEQTRQALGLNVTRTPGKADRVNLLGSKVEEGNKKTERQRREMLKEYMDHPRVQETR 250

Query: 111 KKLDEEAE 118
K+D +AE
Sbjct: 251 DKVDRDAE 258

┌>gi|17508897|ref|NP_492564.1| **L** (NM_060163) T05F1.11.p [Caenorhabditis elegans]
gi|7507212|pir|T24545 hypothetical protein T05F1.11 - Caenorhabditis elegans
gi|3924855|emb|CAB04699.1| (Z81586) predicted using Genefinder-contains similar
domain: PF00646 (F-box domain.), Score=37.6,
E-value=9.2e-08, N=1-cDNA EST yk579e12.3 comes from this
gene-cDNA EST yk579e12.5 comes from this gene
[Caenorhabditis elegans]
Length = 1003

Score = 35.4 bits (80), Expect = 0.30

Identities = 18/45 (40%), Positives = 28/45 (62%), Gaps = 1/45 (2%)

Query: 86 KLPESERRRRMLEQYMNLEKVKKLRKKLDEEAEARAKYIEGEFCK 130
KL E E+R+LE+ M +++ K K+ EAE R K + E K+
Sbjct: 792 KLKEEEKRKRVL EEEEMEMKR-KNEEAKIKLEAEMREKAEQAEIKR 835

┌>gi|19115578|ref|NP_594666.1| (NC_003424) putative DNA repair protein [Schizosaccharomyces pombe]
gi|7492536|pir|T37672 probable DNA repair protein - fission yeast (Schizosaccharomyces pombe)
gi|6138896|emb|CAB59685.1| (AL132675) putative DNA repair protein [Schizosaccharomyces pombe]
Length = 1375

Score = 34.3 bits (77), Expect = 0.61

Identities = 21/54 (38%), Positives = 30/54 (54%), Gaps = 10/54 (18%)

Query: 69 RAAAVQARLNAWVAEGNKLPESERRRRMLEQYMNLEKVKKLRKKLDEEAEARAK 122
R AAV +N +V+ E+E LE+Y +E +KK K LD++AE R K
Sbjct: 842 RVAAVSGTINTFVSH-----ETE-----LEKYKLIESIKKSEKSLDKQAEERDK 885

┌>gi|20349350|ref|XP_112453.1| **L** (XM_112453) similar to hypothetical protein F
Length = 4600

Score = 32.3 bits (72), Expect = 2.9

Identities = 22/61 (36%), Positives = 31/61 (50%), Gaps = 9/61 (14%)

Query: 91 ERRRRMLEQYMNLEKVKKLRKKLDEEAEARAKYIEGEFK---KNPHWGPLKAENPLLPFA 147
ER++R LE+ + KKL+++L+ + E E E K K P GP E P L A
Sbjct: 1027 ERKVDPEPLAVEMOEKVKYQOEPEQVE ERKVDPEPLAVEMOEKVKYQOEPEQVE 1027

Query: 148 Q 148
Q
Sbjct: 1981 Q 1981

└─>gi|20888303|ref|XP_146514.1| **L** (XM_146514) similar to hypothetical protein F
Length = 3053

Score = 32.0 bits (71), Expect = 2.9
Identities = 22/61 (36%), Positives = 31/61 (50%), Gaps = 9/61 (14%)

Query: 91 ERRRRMLEQYMNLEKVKLRKKLDDEEAERAKYIEGEFK---KNPHWGPLKAENPLLPFA 147
ER++R LE+ + KKL+++L+ + E E E K K P GP E P L A
Sbjct: 380 ERKKRELERLAKEMQEKKLQQLERQKE-----EDELKRKVKRKPAGPAAKEEPPLKKA 433

Query: 148 Q 148
Q
Sbjct: 434 Q 434

└─>gi|20837540|ref|XP_130281.1| **L** (XM_130281) similar to oxysterol-binding prot
OSBP-related protein 6 [Mus musculus]
Length = 820

Score = 31.2 bits (69), Expect = 5.3
Identities = 25/85 (29%), Positives = 41/85 (47%), Gaps = 7/85 (8%)

Query: 64 RSTPGRAAAVQARLNAWVAEGNKLPESERRRRMLEQYMNLEKVKLRKKLDDEEAERAKY 123
R P + + L A AE ++ E +R RR + NLE + K KK+ +A R +
Sbjct: 738 RFRPDQRFLEEGNLEAAAAEKQVVEELQSRRRRYMEENNLEHIPKFFKKVI-DANQREAW 796

Query: 124 IEG----EFKKNPHWGPLKAENPLL 144
+ E +K+P G K ++P+L
Sbjct: 797 VSNDTYWELRKDP--GFSKVDSPVL 819

└─>gi|12025422|gb|AAG45917.1|AF309776.1 (AF309776) guanylyl cyclase [Heterodera
Length = 949

Score = 30.8 bits (68), Expect = 7.8
Identities = 19/64 (29%), Positives = 34/64 (52%), Gaps = 10/64 (15%)

Query: 78 NAWVAEGNKLPESERRRRMLEQY-----MNL-----EKVKLRKKLDDEEAERAKYIEGE 127
+ WV ++ P E+ R+ L Q +NL + +++ KL+EE + R K +EGE
Sbjct: 646 DCWVETPSEPTIEKVRQKLQMGARRVNLMDHVFDMLEQYANKLEEEVQERTKELEGE 705

Query: 128 FKKN 131
+K+
Sbjct: 706 KRKS 709

└─>gi|6739527|gb|AAF27289.1|AF140613.1 (AF140613) N-hydroxylating cytochrome P4
Length = 542

Score = 30.4 bits (67), Expect = 8.9
Identities = 22/80 (27%), Positives = 36/80 (44%)

Query: 82 DRRMLEQYMNLEKVKLRKKLDDEEAERAKYIEGEFK---KNPHWGPLKAENPLLPFA 147

R+ + + ++ + K L K EEA+ YI +FK N + A R+
 Sbjct: 158 RKILTSEIISPARKWLHDKRAEEADNLVFIHNQFKANKNVNLRATATRYGGNVIRKRV 217
 Query: 153 EAYRRFGRGAPSAGPLREKM 172
 + R FG+G P GP E++
 Sbjct: 218 FSKRYFGKMPDGGPGPEEI 237

Genselectedsequences Selectall Deselectall

Database: All non-redundant GenBank CDS
 translations+PDB+SwissProt+PIR+PRF
 Posted date: Sep 4, 2002 12:20 AM
 Number of letters in database: 330,426,180
 Number of sequences in database: 1,044,513

Lambda K H
 0.313 0.130 0.379

Gapped
 Lambda K H
 0.267 0.0410 0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Hits to DB: 109,376,468
 Number of Sequences: 1044513
 Number of extensions: 3934752
 Number of successful extensions: 13080
 Number of sequences better than 10.0: 53
 Number of HSP's better than 10.0 without gapping: 10
 Number of HSP's successfully gapped in prelim test: 43
 Number of HSP's that attempted gapping in prelim test: 13046
 Number of HSP's gapped (non-prelim): 74
 length of query: 178
 length of database: 330,426,180
 effective HSP length: 113
 effective length of query: 65
 effective length of database: 212,396,211
 effective search space: 13805753715
 effective search space used: 13805753715
 T: 11
 A: 40
 X1: 16 (7.2 bits)
 X2: 38 (14.6 bits)
 X3: 64 (24.7 bits)
 S1: 42 (21.9 bits)
 S2: 67 (30.4 bits)



Nucleotide

Protein

protein-protein

Translations

BLASTRetrieve results for an
RIDSearch

MAVFEKNTRPKIAMVGSGMIGGTMAFLCSLRELGDVVLFDVVPNMPMGKAMDISHNSS
VV
DTGITVYGSNSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAI
KS
YCPNAFVINITNPLDVMVAALQESSGLPHHRICGMAGMLDSSRFRRMIADKLEVS PRD

Set subsequence From: To: Choose database Do CD-Search ☒Now: **BLAST!** or **Options** for advanced blastingLimit by entrez or select from: Composition-
based statistics ☒Choose filter ☒ Low complexity ☐ Mask for lookup table only ☐ Mask lower caseExpect Word Size Matrix Gap Costs PSSMOther advanced PHI pattern

Ap 9

FormatShow ☒ Graphical Overview ☒ Linkout ☒ NCBI-gi Alignment ☒ in HTML ☒ formatNumber of: Descriptions ☒ Alignments ☒Alignment view ☒Format for PSI-BLAST ☐ with inclusion threshold: Limit results by or select from: ☒Expect value range: Layout: ☒ Formatting options on page with results: ☒Autoformat ☒**BLAST!** or **Reset all**Get the URL with preset values ? **Get URL**



Nucleotide

Protein

formatting **BLAST**

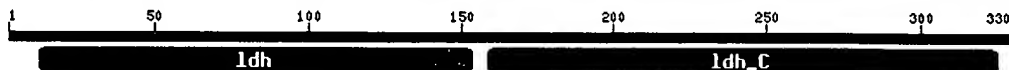
Translations

Retrieve results for an
RID

Your request has been successfully submitted and put into the Blast Queue.

Query = (330 letters)

Putative conserved domains have been detected, click on the image below for detailed results.



The request ID is 1031904433-0681-18522

Format! or **Reset all**

The results are estimated to be ready in 7 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show ☒ Graphical Overview ☒ Linkout ☒ NCBI-gi ☒ Alignment ☒ in format

Number of: Descriptions Alignments

Alignment view

Format for PSI-BLAST ☐ with inclusion threshold:

Limit results by or select from:

Expect value range:



NCBI Conserved Domain Search

[New Search](#)
[PubMed](#)
[Nucleotide](#)
[Protein](#)
[Structure](#)
[CDD](#)
[Taxonomy](#)
[Help?](#)

RPS-BLAST 2.2.3 [Apr-24-2002]

Query= local sequence:
(330 letters)

Database: oasis_sap.v1.58
4540 PSSMs; 885,521 total columns

Click on boxes for multiple alignments



Domain Relatives

- .. This CD alignment includes 3D structure. To display structure, download [Cn3D!](#)

PSSMs producing significant alignments:

Score E
(bits) value

- [gnl|CDD|4825](#) pfam02866, ldh_C, lactate/malate dehydrogenase, alpha/beta C-t... [138](#) 2e-34
- [gnl|CDD|5846](#) pfam00056, ldh, lactate/malate dehydrogenase, NAD binding doma... [110](#) 8e-26
- [gnl|CDD|2579](#) pfam02056, Glyco_hydro_4, Family 4 glycosyl hydrolase [40.6](#) 7e-05

- [gnl|CDD|4825](#), pfam02866, ldh_C, lactate/malate dehydrogenase, alpha/beta C-terminal domain. L-lactate dehydrogenases are metabolic enzymes which catalyse the conversion of L-lactate to pyruvate, the last step in anaerobic glycolysis. L-2-hydroxyisocaproate dehydrogenases are also members of the family. Malate dehydrogenases catalyse the interconversion of malate to oxaloacetate. The enzyme participates in the citric acid cycle. L-lactate dehydrogenase is also found as a lens crystallin in bird and crocodile eyes.

CD-Length = 171 residues, 98.8% aligned
Score = 138 bits (350), Expect = 2e-34

```

Query: 158  MLDSRRFRMIADKLEVSPRDVQGMVIGVHGDHVPVLSRYATVNGIPLSEFVK-KGWIKQ 216
Sbjct: 2    RLDSARARTLLAEKLGVDPRSVHVIYIIGEHGDSEVPVWSHANVTGVPLESLVKELGKDS 61

Query: 217  EEVDDIVQKTKVAGGEIVRLGQGSAYYAPGASAIQMAESYLKDRKRMVVCSCYLQGQYG 276
Sbjct: 62   DELEELIERVQDAGYEVKA--KGSTYSIALAGARIAKAILRDTNGVLPVSVYLDGFGY 119

Query: 277  VQNH-YLGVPCVIGGRGVEKIIIELELTAQERQELQGSIDEVKEMQKAI AAL 326
Sbjct: 120  IPDDVYFSPVVLGRNGVEEIVELPLNDFEREKLEKSADELKIIIEKGFAF 170

```

- [gnl|CDD|5846](#), pfam00056, ldh, lactate/malate dehydrogenase, NAD binding domain. L-lactate dehydrogenases are metabolic enzymes which catalyse the conversion of L-lactate to pyruvate,

of the family. Malate dehydrogenases catalyse the interconversion of malate to oxaloacetate. The enzyme participates in the citric acid cycle. L-lactate dehydrogenase is also found as a lens crystallin in bird and crocodile eyes. N-terminus (this family) is a Rossman NAD-binding fold. C-terminus is an unusual alpha+beta fold.

CD-Length = 145 residues, 96.6% aligned
Score = 110 bits (276), Expect = 8e-26

```
Query: 11 KIAMVG-SGMIGGTMAFLCSLRELG-DVVLFDVVPNMPMGKAMDISHNSSVVDTGITVYG 68
Sbjct: 5 KVAVVGAGGGVGSSSLAFALALQGLADELVLDINKDKAEGVAMDLQHGAFLLVPG-IIG 63

Query: 69 SNSYECLKGADVVIITAGITKIPGKSDKEWSRMDLLPVNIKIMREVGAAIKSYCPNAFVI 128
Sbjct: 64 GDDYEALKDADVVIITAGVPRKPGMT-----RLDLLNRNAKIFKDIVPALAKSAPDAIVL 118

Query: 129 NITNPLDVMVAALQESSGLPHHRICG 154
Sbjct: 119 VVSNPVDILTIAWKVSGFPPPERVIG 144
```

[gnl\[CDD\]2579](#), pfam02056, Glyco_hydro_4, Family 4 glycosyl hydrolase.

CD-Length = 416 residues, only 57.0% aligned
Score = 40.6 bits (95), Expect = 7e-05

```
Query: 11 KIAMVGSG---MIGGTMAFLCSLREL--GDVVLFDVVPNM--PMGKAMDISHNSSVVDTG 63
Sbjct: 1 KIVIIGGGSTITPKNLLGDLKRTEELPGRELALYDIDEERLDAIQTLCKKLVD EAGPDIK 60

Query: 64 ITVYGSNSYECLKGADVVIITAGITKIPGKSDKE-----WSRMD 102
Sbjct: 61 FEKT-TDRKEALKDADFVINAIRVGLLPARELDEKIPLRHGVVGTIQETVGPGGIFRGLR 119

Query: 103 LLPVNIKIMREVGAAIKSYCPNAFVINITNPLDVMVAALQESSGLPHHRICGMAGMLDSS 162
Sbjct: 120 TIPVFFDIAK---DMEELCPDAWMLNYTNPAAMVTEAVYRRY--PNIKAIGLCHSPIGI 173

Query: 163 RFRMRIADKLEVSPRDVQGMVIGVHGDH MVPLS--RYATVNGIP-LSEFVKKGWIKQEEV 219
Sbjct: 174 KER--LAKALGLDRDDIRVRVAGL--NHMAWLLEVRVYNGDDLYPKLREEVAQYGKDGQKE 229

Query: 220 DDIVQKTK 227
Sbjct: 230 KNIQGAPW 237
```

Sequences producing significant alignments:		Score (bits)	E Value
gi 2497625 sp Q27797 LDH_TOXGO	L-lactate dehydrogenase (LDH... (U35118)	422	e-117
gi 1695772 gb AAC47443.1	lactate dehydrogenase [T... (NC_003317)	364	e-100
gi 17986421 ref NP_539055.1	MALATE DEHYDROGENA... (NC_002696)	337	9e-92
gi 16127885 ref NP_422449.1	malate dehydrogena... (NC_002696)	327	1e-88
gi 2554656 pdb 1LDG	Plasmodium Falciparum L-Lactate Dehyd...	327	2e-88
gi 2497624 sp Q27743 LDH1_PLAFD	L-lactate dehydrogenase (LD... Chain A, Chloroquine Binds In The Cof...	326	3e-88
gi 4699811 pdb 1CEQ A	Chain A, Chloroquine Binds In The Cof...	325	6e-88
gi 3183070 sp O33525 MDH_RHILV	MALATE DEHYDROGENASE >gi 262...	320	1e-86
gi 13094954 gb AAK12097.1	(AF323520) lactate dehydrogenase...	317	1e-85
gi 15966809 ref NP_387162.1	(NC_003047) PROBABLE MALATE DE...	316	3e-85
gi 15889894 ref NP_355575.1	(NC_003062) AGR_C_4782p [Agrob...	315	6e-85
gi 17936514 ref NP_533304.1	(NC_003304) malate dehydrogena...	313	2e-84
gi 15214056 sp P93052 LDH_BOTBR	L-lactate dehydrogenase (LD... (NC_002678)	304	9e-82
gi 13473642 ref NP_105210.1	malate dehydrogena... (NC_003103)	302	4e-81
gi 15892443 ref NP_360157.1	malate dehydrogena... (NC_000963)	298	7e-80
gi 15604243 ref NP_220759.1	MALATE DEHYDROGENA... (NC_000964)	293	3e-78
gi 16079964 ref NP_390790.1	malate dehydrogena... (AF274310)	280	1e-74
gi 10444017 gb AAG17668.1 AF274310.1	lactate deh... (AF274310)	275	4e-73
gi 2497856 sp Q59202 MDH_BACIS	MALATE DEHYDROGENASE >gi 743...	275	8e-73
gi 7387870 sp Q9X4K8 MDH_BACTC	MALATE DEHYDROGENASE >gi 473...	270	2e-71
gi 15615720 ref NP_244024.1	(NC_002570) malate dehydrogena...	266	2e-70
gi 21402635 ref NP_658620.1	(NC_003995) ldh, lactate/malat...	265	5e-70
gi 13541928 ref NP_111616.1	(NC_002689) Malate dehydrogena...	255	6e-67
gi 16081997 ref NP_394412.1	(NC_002578) probable malate de...	244	1e-63
gi 21228068 ref NP_633990.1	(NC_003901) Malate dehydrogena...	243	2e-63
gi 2506848 sp P80040 MDH_CHLAU	MALATE DEHYDROGENASE >gi 201...	241	6e-63
gi 22405888 gb ZP_00000751.1	(NZ_AAAA01000052) hypothetica...	241	1e-62
gi 21674327 ref NP_662392.1	(NC_002932) malate dehydrogena...	237	2e-61
gi 20149959 pdb 1GV0 A	Chain A, Structural Basis For Thermo...	236	4e-61
gi 20149955 pdb 1GUZ A	Chain A, Structural Basis For Thermo...	230	2e-59
gi 3183534 sp P80038 MDH_CHLVI	MALATE DEHYDROGENASE >gi 176...	229	5e-59
gi 20149961 pdb 1GV1 A	Chain A, Structural Basis For Thermo...	228	1e-58
gi 16331672 ref NP_442400.1	(NC_000911) 2-ketoacid dehydro...	225	7e-58
gi 20089703 ref NP_615778.1	(NC_003552) malate dehydrogena...	223	3e-57
gi 15606841 ref NP_214221.1	(NC_000918) malate dehydrogena...	220	2e-56
gi 17231814 ref NP_488362.1	(NC_003272) malate dehydrogena...	219	4e-56
gi 15606767 ref NP_214147.1	(NC_000918) malate dehydrogena...	211	1e-53
gi 14600880 ref NP_147405.1	(NC_000854) malate dehydrogena...	209	3e-53
gi 18313295 ref NP_559962.1	(NC_003364) malate dehydrogena...	197	1e-49
gi 15672358 ref NP_266532.1	(NC_002662) L-lactate dehydrog...	180	2e-44
gi 80325 pir A25805	L-lactate dehydrogenase (EC 1.1.1.27) ...	177	1e-43
gi 16799319 ref NP_469587.1	(NC_003212) similar to L-lacta...	176	3e-43
gi 2506808 sp P13714 LDH_BACSU	L-lactate dehydrogenase (L-LDH)	176	3e-43
gi 16077374 ref NP_388187.1	(NC_000964) L-lactate dehydrog...	176	4e-43
gi 16802256 ref NP_463741.1	(NC_003210) similar to L-lacta...	176	5e-43
gi 126059 sp P00345 LDH_BACME	L-lactate dehydrogenase (L-LD...	174	1e-42
gi 126053 sp P14561 LDHP_BACPS	L-lactate dehydrogenase P (L...	171	1e-41
gi 21397481 ref NP_653466.1	(NC_003995) ldh, lactate/malat...	171	1e-41
gi 21402918 ref NP_658903.1	(NC_003995) ldh_C, lactate/mal...	170	2e-41
gi 15893559 ref NP_346908.1	(NC_003030) L-lactate dehydrog...	169	5e-41
gi 126054 sp P20619 LDHX_BACPS	L-lactate dehydrogenase X (L...	167	2e-40
gi 21399802 ref NP_655787.1	(NC_003995) ldh, lactate/malat...	166	3e-40
gi 17367583 sp Q59244 LDH_BACCL	L-lactate dehydrogenase (L-...	166	5e-40
gi 230128 pdb 1LLC	L-Lactate Dehydrogenase (E.C.1.1.1.27)...	165	7e-40
gi 80070 pir S00019	L-lactate dehydrogenase (EC 1.1.1.27) ...	164	1e-39
gi 11251151 pir T44580	lactate dehydrogenase [imported] - ...	163	2e-39
gi 1730106 sp P50934 LDH_LACSK	L-lactate dehydrogenase (L-L...	163	3e-39



Creation date: 12-15-2003
Indexing Officer: TLO - TRUC P LO
Team: OIPEBackFileIndexing
Dossier: 09390846

Legal Date: 05-15-2003

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Remarks:

Order of re-scan issued on